

## SEQUENCE LISTING

<110> HIZAKI, NORIYUKI  
YASOHARA, YOSHIHIKO  
HASEGAWA, JUNZO

<120> NOVEL CARBONYL REDUCTASE, GENE THEREFOR, AND METHOD OF USING THE SAME

<130> 025835/0104

<140> 10/088,920

<141> 2002-06-03

<150> PCT/JP01/06619

<151> 2001-08-01

<150> JP 2000-232756

<151> 2000-08-01

<160> 11

<210> 1

<211> 277

<212> PRT

<213> Micrococcus luteus

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Gln	Gly	Thr	Trp	Gly	Trp	Gly	Glu	Asp	Pro	Gly	Arg	Arg	Gly	Asp	Glu
			20					25						30	
Val	Ala	Ala	Leu	His	Ala	Gly	Leu	Glu	Leu	Gly	Met	Thr	Leu	Val	Asp
		35					40					45			
Thr	Ala	Glu	Met	Tyr	Ala	Asp	Gly	Gly	Ala	Glu	Glu	Val	Ala	Gly	Glu
		50				55						60			
Ala	Leu	Ala	Gly	Arg	Arg	Asp	Glu	Ala	Phe	Val	Val	Ser	Lys	Val	Met
	65				70					75					80
Pro	Ser	His	Ala	Ser	Arg	Ser	Gly	Thr	Ile	Ala	Ala	Cys	Glu	Arg	Ser
				85					90					95	
Leu	Lys	Arg	Leu	Gly	Thr	Asp	Arg	Ile	Asp	Leu	Tyr	Leu	Leu	His	Trp
			100					105						110	
Gln	Gly	Arg	Tyr	Pro	Leu	Gln	Asp	Thr	Val	Ala	Ala	Phe	His	Gln	Ile
			115					120					125		
Val	Glu	Asp	Gly	Lys	Ile	Arg	Tyr	Trp	Gly	Val	Ser	Asn	Phe	Asp	His
			130				135					140			
Arg	Ala	Leu	Ala	Glu	Leu	Gln	Asp	Val	Pro	Gly	Thr	Ser	Gly	Leu	Thr
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Thr Asp Gln Val Leu Tyr Asn Leu Ser Arg Arg Gly Pro Glu Tyr Asp  
165 170 175

Leu Leu Pro Trp Cys Ala Asp His Gln Leu Pro Val Met Ala Tyr Ser  
180 185 190

Pro Ile Glu Gln Gly Arg Ile Leu Asp Asp Thr Thr Leu Asn Asp Val  
195 200 205

Ala Ala Arg His Ser Val Ser Pro Ala Ala Ala Ala Leu Ala Trp Val  
210 215 220

Leu Arg Arg Asp Ser Leu Cys Thr Ile Pro Lys Ala Ser Ser Pro Gln  
225 230 235 240

His Val Arg Asp Asn Ala Thr Ala Leu Asp Val Glu Leu Thr Arg Glu  
245 250 255

Asp Leu Asp Ala Leu Asp Arg Ala Phe Pro Pro Pro Ser Gly Pro Arg  
260 265 270

Pro Leu Glu Met Leu  
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<212> DNA

<213> Micrococcus luteus

<220>

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<222> (108)..(938)

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ctcagcccac gtcccgcctc aggacaacca gaaggaagtg atcgagg atg cga cgg 116  
Met Arg Arg  
1

atg acg ctg ccg agt ggg gag tcc atc cct gtg ctg ggc cag ggc acc 164  
Met Thr Leu Pro Ser Gly Glu Ser Ile Pro Val Leu Gly Gln Gly Thr  
5 10 15

ggg ggc tgg ggt gag gac ccc ggc cgc cgc ggc gac gag gtc gcc gcg 212  
Trp Gly Trp Gly Glu Asp Pro Gly Arg Arg Gly Asp Glu Val Ala Ala  
20 25 30 35

ctg cac gcc ggc ctc gaa ctg ggc atg acg ctg gtc gac acc gcc gag 260  
Leu His Ala Gly Leu Glu Leu Gly Met Thr Leu Val Asp Thr Ala Glu  
40 45 50

atg tac gcc gac ggc ggt gcg gag gag gtg gct ggt gaa gca ttg gcg 308  
Met Tyr Ala Asp Gly Gly Ala Glu Glu Val Ala Gly Glu Ala Leu Ala  
55 60 65

ggt cgc cgc gac gag gcg ttc gtg gtc agc aag gtc atg ccg tcc cac 356  
 Gly Arg Arg Asp Glu Ala Phe Val Val Ser Lys Val Met Pro Ser His  
           70                          75                          80

gcc tcc cgt tcc ggc acg atc gcg gcc tgc gaa cgc agc ctg aaa cgc 404  
 Ala Ser Arg Ser Gly Thr Ile Ala Ala Cys Glu Arg Ser Leu Lys Arg  
           85                          90                          95

ctg ggc acc gat cgg atc gac ctc tac ctg ctg cac tgg cag ggc agg 452  
 Leu Gly Thr Asp Arg Ile Asp Leu Tyr Leu Leu His Trp Gln Gly Arg  
           100                          105                          110                          115

tac ccg ctg cag gac acc gtc gcg gcc ttc cac cag ctc gtc gag gac 500  
 Tyr Pro Leu Gln Asp Thr Val Ala Ala Phe His Gln Leu Val Glu Asp  
                           120                          125                          130

ggg aaa atc cga tac tgg ggc gtc agc aac ttc gac cac cgg gcc ctc 548  
 Gly Lys Ile Arg Tyr Trp Gly Val Ser Asn Phe Asp His Arg Ala Leu  
                           135                          140                          145

gcc gag ctg cag gac gtg ccg ggc acc agc ggg ctg acc acg gat cag 596  
 Ala Glu Leu Gln Asp Val Pro Gly Thr Ser Gly Leu Thr Thr Asp Gln  
           150                          155                          160

gtg ctg tac aac ctg tcc cgg cga gga ccg gag tac gac ctg ctg ccg 644  
 Val Leu Tyr Asn Leu Ser Arg Arg Gly Pro Glu Tyr Asp Leu Leu Pro  
           165                          170                          175

tgg tgc gcc gac cac cag ctg ccg gtc atg gcg tac tcc ccg atc gag 692  
 Trp Cys Ala Asp His Gln Leu Pro Val Met Ala Tyr Ser Pro Ile Glu  
           180                          185                          190                          195

cag ggc cgc atc ctt gac gac acg acg ctg aac gac gtc gcg gcc cgt 740  
 Gln Gly Arg Ile Leu Asp Asp Thr Thr Leu Asn Asp Val Ala Ala Arg  
                           200                          205                          210

cac agc gtc agc ccc gcg gcg gcg gcc ctt gcc tgg gtg ctg cgc cgc 788  
 His Ser Val Ser Pro Ala Ala Ala Ala Leu Ala Trp Val Leu Arg Arg  
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gac tcc ctc tgc acg atc ccc aag gcg agc agc ccg cag cac gtg cgc 836  
 Asp Ser Leu Cys Thr Ile Pro Lys Ala Ser Ser Pro Gln His Val Arg  
           230                          235                          240

gac aac gcc aca gca ctg gac gtg gag ctg acc cgc gaa gac ctg gat 884  
 Asp Asn Ala Thr Ala Leu Asp Val Glu Leu Thr Arg Glu Asp Leu Asp  
           245                          250                          255

gct ctg gac cgt gcg ttt ccg tcc ccg agc gga ccg cga cca ctg gag 936  
 Ala Leu Asp Arg Ala Phe Pro Pro Pro Ser Gly Pro Arg Pro Leu Glu  
           260                          265                          270                          275

atg ctg tgaccctgcc ccaggcgca gcccggtcgg tccggggcggg ccgggcagtc 988  
 Met Leu

cgggcagcgc tccggtcagc gcaagtctcc gaaggacctg cctgtcacct cctcctgaac 1048

ctgtgcacgc catccatcga ctcccttctcc cgagccctgt cgggttcgcg gtaggcgctg 1108

atcatccgct ggcaggtecc ccaagtggcc tcgagccggg cctctgctt gtcggtgagc 1168  
 aaccgggttc cggcgtgcag ggttcgacgg gcgagtaga gcggtcgcc cgtgcggccg 1228  
 cggtgccat gcaggtectg ctggacccgg cggtggcagc ggaccaacgc gtcgccggct 1288  
 aaccggactg cgagcgaccg gcgttggtga cgcagacgac ctggacactg ggccgtgcgg 1348  
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 tc 1410

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<220>  
 <223> Description of Artificial Sequence: Primer

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 <221> modified\_base  
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 <223> a, t, c, g, other or unknown

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 <221> modified\_base  
 <222> (9)  
 <223> a, t, c, g, other or unknown

<400> 3  
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<210> 4  
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<400> 4  
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<210> 5  
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 <212> DNA  
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<220>  
 <223> Description of Artificial Sequence: Primer

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<210> 9  
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 <212> DNA  
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<220>  
 <223> Description of Artificial Sequence: Synthetic  
 double-stranded DNA

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gttttaggtc aaggtagctt yggttggggg gaagatccag gtcgtcgtgg tgatgaagtt 120  
gctgctttac atgctggtct cgag 144

<210> 10  
<211> 33  
<212> DNA  
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<220>  
<223> Description of Artificial Sequence: Primer

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<210> 11  
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